

#12



PCT

RAW SEQUENCE LISTING

DATE: 06/30/2004

PATENT APPLICATION: US/09/554,960

TIME: 13:03:05

Input Set : A:\Nih342-1.app

Output Set: N:\CRF4\06302004\I554960.raw

3 <110> APPLICANT: Kaslow, David C.
4 Tsuboi, Takafumi
5 Torii, Motomi
6 The Government of the United States of America
7 as represented by the Secretary of the
8 Department of Health and Human Services
10 <120> TITLE OF INVENTION: Vaccines for Blocking Transmission of Plasmodium vivax
12 <130> FILE REFERENCE: 015280-34210US
14 <140> CURRENT APPLICATION NUMBER: US 09/554,960
C--> 15 <141> CURRENT FILING DATE: 2000-05-22
17 <150> PRIOR APPLICATION NUMBER: US 60/045,283
18 <151> PRIOR FILING DATE: 1997-05-01
20 <150> PRIOR APPLICATION NUMBER: WO PCT/US98/25742
21 <151> PRIOR FILING DATE: 1998-12-04
23 <160> NUMBER OF SEQ ID NOS: 24
25 <170> SOFTWARE: PatentIn Ver. 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1066
29 <212> TYPE: DNA
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34 <222> LOCATION: (147)..(857)
35 <223> OTHER INFORMATION: Pvs28
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40 ttatacaaaa acgactcccc ctttgagata acacccaact gagctcgatt cccctcccc 120
42 acttttgctc ctcccccttg ttcaaaa atg aat acc tac cac agc ttg ctg ttc 173
43 Met Asn Thr Tyr His Ser Leu Leu Phe
44 1 5
46 ctt ctg gcc atc gtg ctt act gtt aag cac acc ttc gca aag gtc acc 221
47 Leu Leu Ala Ile Val Leu Thr Val Lys His Thr Phe Ala Lys Val Thr
48 10 15 20 25
50 gcg gag acc caa tgc aaa aat ggc tat gta gtc caa atg agc aat cat 269
51 Ala Glu Thr Gln Cys Lys Asn Gly Tyr Val Val Gln Met Ser Asn His
52 30 35 40
54 ttt gaa tgc aaa tgc aac gac ggg ttt gtt atg gca aat gaa aac act 317
55 Phe Glu Cys Lys Cys Asn Asp Gly Phe Val Met Ala Asn Glu Asn Thr
56 45 50 55
58 tgc gag gaa aaa cgc gat tgc aca aat cca caa aat gta aat aaa aac 365
59 Cys Glu Glu Lys Arg Asp Cys Thr Asn Pro Gln Asn Val Asn Lys Asn
60 60 65 70
62 tgt gga gac tac gct gtg tgt gca aac acc aga atg aat gat gag gaa 413

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64      75      80      85
66 aga gca tta cga tgc ggc tgc ata tta ggg tac acc gta atg aat gag 461
67 Arg Ala Leu Arg Cys Gly Cys Ile Leu Gly Tyr Thr Val Met Asn Glu
68 90      95      100      105
70 gtg tgt act cca aat aaa tgt aac ggc gtt ttg tgt gga aag gga aag 509
71 Val Cys Thr Pro Asn Lys Cys Asn Gly Val Leu Cys Gly Lys Gly Lys
72      110      115      120
74 tgc atc tta gat ccc gct aat gtg aac agc acc atg tgc tct tgt aat 557
75 Cys Ile Leu Asp Pro Ala Asn Val Asn Ser Thr Met Cys Ser Cys Asn
76      125      130      135
78 ata gga acc aca ttg gat gaa tct aaa aaa tgt gga aag cca gga aaa 605
79 Ile Gly Thr Thr Leu Asp Glu Ser Lys Lys Cys Gly Lys Pro Gly Lys
80      140      145      150
82 act gaa tgc acg ttg aag tgt aag gca aac gaa gaa tgt aaa gag act 653
83 Thr Glu Cys Thr Leu Lys Cys Lys Ala Asn Glu Glu Cys Lys Glu Thr
84      155      160      165
86 cag aat tat tac aag tgc gtt gcg aag gga agc ggc gga gaa ggc agc 701
87 Gln Asn Tyr Tyr Lys Cys Val Ala Lys Gly Ser Gly Gly Glu Gly Ser
88 170      175      180      185
90 ggt gga gaa ggc agc ggc gga gag ggc agc ggc gga gag ggc agc ggc 749
91 Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly
92      190      195      200
94 gga gag ggc agc ggt gga gac aca gga gca gct tac agt ctc atg aac 797
95 Gly Glu Gly Ser Gly Gly Asp Thr Gly Ala Ala Tyr Ser Leu Met Asn
96      205      210      215
98 gga tct gca gta atc agc ata cta ctt gta ttc gcc ttc ttc atg atg 845
99 Gly Ser Ala Val Ile Ser Ile Leu Leu Val Phe Ala Phe Phe Met Met
100      220      225      230
102 tca tta gtg tagacgattc tacacacaca cacaaacata cacaagggga 894
103 Ser Leu Val
104      235
106 gaagcgtctc acagagtcag ttcaagtcac acgcacaaaa aaggaaagta catccagctg 954
108 gtgaaagagc atttatgtgt gcagttatcc ttgggagaag caccctccac ccagttgcgt 1014
110 tgctgttacc ttaaaactta gtggcaccga tatcgaattt gactttgctc gc 1066
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114 <211> LENGTH: 236
115 <212> TYPE: PRT
116 <213> ORGANISM: Plasmodium vivax
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122 Val Lys His Thr Phe Ala Lys Val Thr Ala Glu Thr Gln Cys Lys Asn
123      20      25      30
125 Gly Tyr Val Val Gln Met Ser Asn His Phe Glu Cys Lys Cys Asn Asp
126      35      40      45
128 Gly Phe Val Met Ala Asn Glu Asn Thr Cys Glu Glu Lys Arg Asp Cys
129      50      55      60
131 Thr Asn Pro Gln Asn Val Asn Lys Asn Cys Gly Asp Tyr Ala Val Cys

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132 65              70              75              80
134 Ala Asn Thr Arg Met Asn Asp Glu Glu Arg Ala Leu Arg Cys Gly Cys
135              85              90              95
137 Ile Leu Gly Tyr Thr Val Met Asn Glu Val Cys Thr Pro Asn Lys Cys
138              100             105             110
140 Asn Gly Val Leu Cys Gly Lys Gly Lys Cys Ile Leu Asp Pro Ala Asn
141              115             120             125
143 Val Asn Ser Thr Met Cys Ser Cys Asn Ile Gly Thr Thr Leu Asp Glu
144              130             135             140
146 Ser Lys Lys Cys Gly Lys Pro Gly Lys Thr Glu Cys Thr Leu Lys Cys
147 145             150             155             160
149 Lys Ala Asn Glu Glu Cys Lys Glu Thr Gln Asn Tyr Tyr Lys Cys Val
150              165             170             175
152 Ala Lys Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly
153              180             185             190
155 Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Glu Gly Ser Gly Gly Asp
156              195             200             205
158 Thr Gly Ala Ala Tyr Ser Leu Met Asn Gly Ser Ala Val Ile Ser Ile
159              210             215             220
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162 225             230             235
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166 <211> LENGTH: 995
167 <212> TYPE: DNA
168 <213> ORGANISM: Plasmodium vivax
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172 <222> LOCATION: (255)..(914)
173 <223> OTHER INFORMATION: Pvs25
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178 tttcgattgt ttgcttgttt gctttttttgc ttattcgccc gtttttccgc ttgcccgttc 120
180 gcccgctcca caacgcgccg ctgcaaagggt tgcccaccac cgaccacaaa aacttattca 180
182 ccaccatccg agcggaaagg aacgccgccc actgtgctgc ctacctcccc gaataacaac 240
184 tccacttagc caaa atg aac tcc tac tac agc ctc ttc gtt ttt ttc ctc 290
185              Met Asn Ser Tyr Tyr Ser Leu Phe Val Phe Phe Leu
186              1              5              10
188 gtc caa att gcg cta aag tat agc aag gca gcc gtc acg gta gac acc 338
189 Val Gln Ile Ala Leu Lys Tyr Ser Lys Ala Ala Val Thr Val Asp Thr
190              15              20              25
192 ata tgc aaa aat gga cag ctg gtt caa atg agt aac cac ttt aag tgt 386
193 Ile Cys Lys Asn Gly Gln Leu Val Gln Met Ser Asn His Phe Lys Cys
194              30              35              40
196 atg tgt aac gaa ggg ctg gtg cac ctt tcc gaa aat aca tgt gaa gaa 434
197 Met Cys Asn Glu Gly Leu Val His Leu Ser Glu Asn Thr Cys Glu Glu
198 45              50              55              60
200 aaa aat gaa tgc aag aaa gaa acc cta ggc aaa gca tgc ggg gaa ttt 482
201 Lys Asn Glu Cys Lys Lys Glu Thr Leu Gly Lys Ala Cys Gly Glu Phe
202              65              70              75

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204 ggc cag tgt ata gaa aac cca gac cca gca cag gta aac atg tac aaa 530
205 Gly Gln Cys Ile Glu Asn Pro Asp Pro Ala Gln Val Asn Met Tyr Lys
206      80      85      90
208 tgt ggt tgc att gag ggc tac act ttg aag gaa gac act tgt gtg ctt 578
209 Cys Gly Cys Ile Glu Gly Tyr Thr Leu Lys Glu Asp Thr Cys Val Leu
210      95      100      105
212 gat gta tgt caa tac aaa aat tgt gga gaa agt ggc gaa tgc att gtt 626
213 Asp Val Cys Gln Tyr Lys Asn Cys Gly Glu Ser Gly Glu Cys Ile Val
214      110      115      120
216 gag tac ctc tcg gaa atc caa agt gca ggt tgc tca tgt gct att ggc 674
217 Glu Tyr Leu Ser Glu Ile Gln Ser Ala Gly Cys Ser Cys Ala Ile Gly
218 125      130      135      140
220 aaa gtc ccc aat cca gaa gat gag aaa aaa tgt acc aaa acg gga gaa 722
221 Lys Val Pro Asn Pro Glu Asp Glu Lys Lys Cys Thr Lys Thr Gly Glu
222      145      150      155
224 act gct tgt caa ttg aaa tgt aac aca gat aat gaa gtc tgc aaa aat 770
225 Thr Ala Cys Gln Leu Lys Cys Asn Thr Asp Asn Glu Val Cys Lys Asn
226      160      165      170
228 gtt gaa gga gtt tac aag tgc cag tgt atg gaa ggc ttt acg ttc gac 818
229 Val Glu Gly Val Tyr Lys Cys Gln Cys Met Glu Gly Phe Thr Phe Asp
230      175      180      185
232 aaa gag aaa aat gta tgc ctt tcc tat tct gta ttt aac atc cta aac 866
233 Lys Glu Lys Asn Val Cys Leu Ser Tyr Ser Val Phe Asn Ile Leu Asn
234      190      195      200
236 tac tcc ctc ttc ttt atc atc ctg ctt gtc ctt tcg tac gtc ata 911
237 Tyr Ser Leu Phe Phe Ile Ile Leu Leu Val Leu Ser Tyr Val Ile
238 205      210      215
240 taagtgcgaa acttgccgag ctaagcagcg caaatttttt aagttaaaat acttttcttt 971
242 actgaactta ccgacttggt atgt 995
245 <210> SEQ ID NO: 4
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247 <212> TYPE: PRT
248 <213> ORGANISM: Plasmodium vivax
250 <400> SEQUENCE: 4
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254 Leu Lys Tyr Ser Lys Ala Ala Val Thr Val Asp Thr Ile Cys Lys Asn
255 20 25 30
257 Gly Gln Leu Val Gln Met Ser Asn His Phe Lys Cys Met Cys Asn Glu
258 35 40 45
260 Gly Leu Val His Leu Ser Glu Asn Thr Cys Glu Glu Lys Asn Glu Cys
261 50 55 60
263 Lys Lys Glu Thr Leu Gly Lys Ala Cys Gly Glu Phe Gly Gln Cys Ile
264 65 70 75 80
266 Glu Asn Pro Asp Pro Ala Gln Val Asn Met Tyr Lys Cys Gly Cys Ile
267 85 90 95
269 Glu Gly Tyr Thr Leu Lys Glu Asp Thr Cys Val Leu Asp Val Cys Gln
270 100 105 110
272 Tyr Lys Asn Cys Gly Glu Ser Gly Glu Cys Ile Val Glu Tyr Leu Ser

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276          130          135          140
278 Pro Glu Asp Glu Lys Lys Cys Thr Lys Thr Gly Glu Thr Ala Cys Gln
279 145          150          155          160
281 Leu Lys Cys Asn Thr Asp Asn Glu Val Cys Lys Asn Val Glu Gly Val
282          165          170          175
284 Tyr Lys Cys Gln Cys Met Glu Gly Phe Thr Phe Asp Lys Glu Lys Asn
285          180          185          190
287 Val Cys Leu Ser Tyr Ser Val Phe Asn Ile Leu Asn Tyr Ser Leu Phe
288          195          200          205
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291          210          215
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295 <211> LENGTH: 377
296 <212> TYPE: PRT
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence:Pvs25-Pvs28
301 fusion protein
303 <400> SEQUENCE: 5
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307 Ser Asn His Phe Lys Cys Met Cys Asn Glu Gly Leu Val His Leu Ser
308          20          25          30
310 Glu Asn Thr Cys Glu Glu Lys Asn Glu Cys Lys Lys Glu Thr Leu Gly
311          35          40          45
313 Lys Ala Cys Gly Glu Phe Gly Gln Cys Ile Glu Asn Pro Asp Pro Ala
314          50          55          60
316 Gln Val Asn Met Tyr Lys Cys Gly Cys Ile Glu Gly Tyr Thr Leu Lys
317 65          70          75          80
319 Glu Asp Thr Cys Val Leu Asp Val Cys Gln Tyr Lys Asn Cys Gly Glu
320          85          90          95
322 Ser Gly Glu Cys Ile Val Glu Tyr Leu Ser Glu Ile Gln Ser Ala Gly
323          100          105          110
325 Cys Ser Cys Ala Ile Gly Lys Val Pro Asn Pro Glu Asp Glu Lys Lys
326          115          120          125
328 Cys Thr Lys Thr Gly Glu Thr Ala Cys Gln Leu Lys Cys Asn Thr Asp
329          130          135          140
331 Asn Glu Val Cys Lys Asn Val Glu Gly Val Tyr Lys Cys Gln Cys Met
332 145          150          155          160
334 Glu Gly Phe Thr Phe Asp Lys Glu Lys Asn Val Cys Leu Ser Gly Gly
335          165          170          175
337 Gly Pro Gly Gly Gly Ala Lys Val Thr Ala Glu Thr Gln Cys Lys Asn
338          180          185          190
340 Gly Tyr Val Val Gln Met Ser Asn His Phe Glu Cys Lys Cys Asn Asp
341          195          200          205
343 Gly Phe Val Met Ala Asn Glu Asn Thr Cys Glu Glu Lys Arg Asp Cys
344          210          215          220

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VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/554,960**

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